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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/677,672	10/02/2000	Jean-Christophe Francis Audonnet	454313-3160	3424

20999 7590 06/06/2002  
FROMMER LAWRENCE & HAUG  
745 FIFTH AVENUE- 10TH FL.  
NEW YORK, NY 10151

[REDACTED] EXAMINER

NGUYEN, DAVE TRONG

[REDACTED] ART UNIT [REDACTED] PAPER NUMBER

1632

DATE MAILED: 06/06/2002

6

Please find below and/or attached an Office communication concerning this application or proceeding.



UNITED STATES DEPARTMENT OF COMMERCE  
Patent and Trademark Office

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SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/677,672	10/02/2000	Audonnet	
EXAMINER			
DAVE NGUYEN			
ART UNIT		PAPER NUMBER	
1632		6	

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application.

Commissioner of Patents

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

Applicant is given ONE MONTH from the mailing date of this communication within which to comply with the sequence rules, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136(a). Direct the reply to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the reply.

Any inquiry concerning this communication or earlier communications regarding the formalities should be directed to Patent Analyst Dianiece Jacobs, whose telephone number is (703) 305-3388.

Any inquiry concerning this communication or earlier communications from the

examiner should be directed to examiner *Dave Nguyen* whose telephone number is **(703) 305-2024**.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, *Deborah Reynolds*, may be reached at **(703) 305-4051**.

Papers related to this application may be submitted to Group 1600 by facsimile transmission. Papers should be faxed to Group 1600 via the PTO Fax Center located in Crystal Mall 1. The faxing of such papers must conform with the notice published in the Official Gazette, 1096 OG 30 (November 15, 1989). The CM1 Fax Center number is **(703) 305-7401**.

Any inquiry of a general nature or relating to the status of this application should be directed to the *Group receptionist* whose telephone number is **(703) 308-0196**.

Dave Nguyen  
Primary Examiner  
Art Unit: 1632 

**DAVE T. NGUYEN**  
**PRIMARY EXAMINER**

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- 7. Other: Please see the attached Raw Sequence Listing Error Summary

**Applicant Must Provide:**

- An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY**

1  
No. 1  
D  
**RAW SEQUENCE LISTING  
ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/677,672

Source: O/PE

Date Processed by STIC: 10/13/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin30help@uspto.gov](mailto:patin30help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/672,672

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleic The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".

2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".

3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.

4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 Variable Length Sequence(s) \_\_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

8 Skipped Sequences (OLD RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 Skipped Sequences (NEW RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000

10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 Use of <213>Organism (NEW RULES) Sequence(s) \_\_\_\_\_ are missing this mandatory field or its response.

12 Use of <220>Feature (NEW RULES) Sequence(s) \_\_\_\_\_ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 PatentIn ver. 2.0 "bug" → Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File-Manager" or any other means to copy file to floppy disk.

O I P E

RAW SEQUENCE LISTING DATE: 10/13/2000  
PATENT APPLICATION: US/09/677,672 TIME: 08:27:22

Input Set : A:\Audonne1.app  
Output Set: N:\CRF3\10132000\I677672.raw

Does Not Comply  
Corrected Diskette Needed

pp. 1-5

(global error)

This is a MANDATORY numeric identifier. The only valid responses for C2137 are: Unknown or

Artificial Sequence  
or scientific name  
(genus/species).

See 1.823 of  
new sequence  
Rules. See, also,  
circled portion  
of item 12 on  
Error summary  
sheet.

RAW SEQUENCE LISTING  
PATENT APPLICATION -- US/09/677,672

DATE: 10/13/2000  
TIME: 08:27:22

Input Set : A:\Audonnel.app  
Output Set: N:\CRF3\10132000\I677672.raw

62 gatctaaaga gcaactcaagc agccatagac cagatcaatg gaaaattaaa cagagtgatt 1200  
 63 gaaaggacca atgagaaaatt ccatcaaaa gaaaaggaat tctcagaagt agaagggaga 1260  
 64 atccaggatt tggagaatc tgtagaaagc accaaaatag acctatggtc ctcaaatgc 1320  
 65 gaattgtcg tggctctaga aatcaacat acaattgact taacatgc agaaatgaat 1380  
 66 aattatttcg agaagactag cgcgcagttt agaaaaacg cggaaagacat gggaggtgga 1440  
 67 tggttcaaga ttaccacaa atgtgataat gcatgcattt gatcaataag aatgggaca 1500  
 68 tatgaccattt acatatacag agatgaaca ttaacaacc gattcaaat caaaagtgtt 1560  
 69 gagttgaatc caggctacaa agattggata ctgtggattt cattcgccat atcatgttc 1620  
 70 ttaatttgcg ttgttctattt gggtttcat atgtggcattt gccaaaaagg caacatcagg 1680  
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 72 <210> SEQ ID NO: 4  
 73 <211> LENGTH: 34  
 74 <212> TYPE: DNA  
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 76 <400> SEQUENCE: 4  
 77 ttggatctt actcaaatgc aaatgttca tctg 34  
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 79 <211> LENGTH: 1698  
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 82 <400> SEQUENCE: 5  
 83 ttaaaacaa taactgtat ccaaatttgc gttttttttt gttttttttt 60  
 84 aatccatag gaaaatattt caacaatca tataatgtt tagatgttgc aatttgcaca 120  
 85 ttaatagatc caatgttgc agatcccccac ttgtatgttgc ttcgtatgttgc 180  
 86 ctcttcatag aaaaagcag cgctttcgc aattgttgc accatccatgc 240  
 87 ataaagacaa ccattttttt gataactactg acccattggg tctacagtca aaacccaacc 300  
 88 aatggcaaca acacagccac attatgttgc ggacaccatg ctagacaaaatgc 360  
 89 gtaaaaacaa taactgtat ccaaatttgc gttttttttt gttttttttt 420  
 90 aatccatag gaaaatattt caacaatca tataatgtt tagatgttgc aatttgcaca 480  
 91 ttaatagatc caatgttgc agatcccccac ttgtatgttgc ttcgtatgttgc 540  
 92 ctcttcatag aaaaagcag cgctttcgc aattgttgc accatccatgc 600  
 93 gcatcgccat ggtccattttt aatccatgc tttttttttt tttttttttt 660  
 94 acatggacag gtgtcactca aaacggaaaga agtggagctt gcaaaagggg 720  
 95 agtttcttgc gcccacttgc ttgttgcattt aatccatgc 780  
 96 gtgacaatgc ttacaataaa aattttcacaa aatccatatac tttttttttt tttttttttt 840  
 97 agctcaaaacc aacagcaaac agaattgtac atccaaagaaatc cggagcggat aacagtctca 900  
 98 aaaaaaaagaa gtcaacaaac gataatccctt aatccatgc tttttttttt tttttttttt 960  
 99 caatccggca ggataacgtt atactggacc ttgttgcattt aatccatgc 1020  
 100 aacatcaatgc gcaattttttt tttttttttt tttttttttt tttttttttt 1080  
 101 tctgtatgtt gatccatgc accccatagac aatccatgc tttttttttt tttttttttt 1140  
 102 gaagcatccc caacggacaaa ccattttttt aatccatgc tttttttttt tttttttttt 1200  
 103 ccaatgtatcat cggggatccac actttaaagc tggccacttgc gatggggat tttttttttt 1260  
 104 agccaaatccatc agggatctttt ggaccaatgc cggggatccat aaaaacggc tttttttttt 1320  
 105 tgggtatgg tgggtatgg tttttttttt tttttttttt tttttttttt tttttttttt 1380  
 106 atctaaaaga gcaactcaagc agccatcgac cagattaatgc gaaaattaaa cagagtgattt 1440  
 107 gaaaggacca atgagaaaattt ccatcaaaa gagaaggaaatc tttttttttt tttttttttt 1500  
 108 atccaggactt tggagaatgc tgtagaaagc accaaaatag acctatggtc ctcaaatgc 1560  
 109 gaattgtcg tggctctaga aatcaacat acaattgact taacatgc agaaatgaat 1620  
 110 aattatttcg agaagactag acggccagttt agaaaaacg cggaaagacat gggaggtgga 1680  
 111 tggttcaaga ttaccacaa atgtgataat gcatgcattt gatcaataag aatgggaca 1748  
 112 tatgaccattt acatatacag agatgaaca ttaacaacc gattcaaat caaaagtgtt 1808  
 113 gagttgaatc caggctacaa agattggata ctgtggattt cattcgccat atcatgttc 1868  
 114 ttaatttgcg ttgttctattt gggtttcat atgtggcattt gccaaaaagg caacatcagg 1928

RAW-SEQUENCE LISTING DATE: 10/13/2000  
 PATENT-APPLICATION: US/09/677,672 TIME: 08:27:22

Input Set : A:\Audonne1.app  
 Output Set: N:\CRF3\10132000\I677672.raw

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 118 <210> SEQ ID NO: 6  
 119 <211> LENGTH: 35  
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 126 <210> SEQ ID NO: 7  
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 128 <212> TYPE: DNA  
 W--> 130 <213> ORGANISM:  
 130 <400> SEQUENCE: 7  
 131 tttggatccy tacatcttrt cgatgtcaaa gg 32  
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 135 <211> LENGTH: 1412  
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 141 acaggctcga actgcacgg cgcgcatac agagagtaca atgaaacagt aagagtagaa 180  
 142 agaataccccc atgtgtataa tactgtaca attgtgtaca tagaaagatc ttcaaatggaa 240  
 143 tactacatga acaacacccg accactttgt gaggccccagg gctttgcacc attttccaaa 300  
 144 gacaatggaa tacgaattgg gtcgagaggg catgtttttg taataagaga accttttgta 360  
 145 tcatgttcgc ctcagaatgt tagaaccttt tccctcacac agggctcatt actcaatgac 420  
 146 aaacatteta acggcacatc ggacggcga agtccatata ggactttgtat gagtgtcaaa 480  
 147 ataggccaat caccataatgt gtatacagct aggtttgtat cgggtggatc gtcaagcaaca 540  
 148 gcatgcccattc atggaaaaaa tggatgacag ttggaggcac agggccgcac aatcaagcag 600  
 149 ttgcagtatg gaactatgtg ggttgcggg ttgtatattat taattcatgg gcatggata 660  
 150 tcttaagaac ccaagaatcg tcatgcaccc gcatggaaagg agactgttat tgggtgtatg 720  
 151 ctgtggacc ggcaaacagg caagctaaat ataggatataa caagcaaaa aatggaaagaa 780  
 152 taattgggca gactgtatata agttcaatgt ggggacacat agaggagtgt tcttggtaacc 840  
 153 ccaatgaagg gaagggtggaa tgcataatgc gggacaactg gactggaaaca aatagaccaa 900  
 154 ttctggtaat atcttcgtat ctatcgatc cagtcggata tttgtgtgc ggcattccca 960  
 155 ctgacactcc tagggggag gatagtcaat tcacaggctc atgtacaacg cctttggaa 1020  
 156 ataaaggata cgggtaaaaa gtttcgggtt ttcgacaagg aactgacgta tggggccggaa 1080  
 157 ggacaatttag taggacttca agatcaggat tgcataatataa aagatcagg aatgggttga 1140  
 158 cacagaaatg taaagatcaa atcagaaggc aagtgtatata tgcataacccaa aatgggttgcag 1200  
 159 gatatacgcc ttcttcaca ttgcgggtt aactaacaaa aagggatgt ttagtccct 1260  
 160 gtttccgggt tgaatgtattt agaggttaac ctgaaacaa aacaatatgg acctctagca 1320  
 161 gtcctattgt gatgtggaa tgcataatataa aagttccag tgggtcatgg cacgtggag 1380  
 162 ctattttcccttgcacatc gataagatgt aa 1412  
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 166 <211> LENGTH: 1414  
 167 <212> TYPE: DNA  
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 169 <400> SEQUENCE: 9  
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 171 aacgtcattc tccatgtagt cagcattata gtaacagtac tggttctcaa taacaatgg 120

RAW SEQUENCE LISTING DATE: 10/13/2000  
PATENT APPLICATION: US/09/677,672 TIME: 08:27:22

Input Set : A:\Audonnel.app  
Output Set: N:\CRF3\10132000\I677672.raw

172 acagggtctga actgcaaagg gacgatcata agagagataca atgaaaacat aagagtagaa 180  
 173 agaattactc aatggtataa taccagtaca attgagtaca tagagagacc ttcaatgaa 240  
 174 tactacatga acaaaccgga accacttggt gaggccccaa gcttgcaccc atttttccaa 300  
 175 gataatggaa tacaatggt gtcgagggc catgtttttg taataaaggaa acctttgtc 360  
 176 tcatgttcgc cctcagaatg tagaacctt ttccctcacac agggctcatc actcaatgac 420  
 177 aacacattcta acggcacagt gaaggaccga agtccatata ggacttigt gagggtcaaa 480  
 178 ataggccat caccataatgt gatcaagct aggtttgaat cggtggatcgt gtcaccaaca 540  
 179 gcatggccat atggaaaaaa atggatgaca gttggatcga caggggccgat taatcaagca 600  
 180 attcgtagt tgaatctatgg aggttgcgttccg gttgatataa ttaatttcatg gcaaggggat 660  
 181 atcttaagaa cccaaagaatc gtcatgcacc tgcattaaag gagactgtta ttgggtgatg 720  
 182 atgtatggac cggcaaatag gcaaggttacat tataaggatat tcaaaaggaa agatggaaaga 780  
 183 aatattggcc agactatgtt aatgtttcaat gggggacacca tagaggatg ttcttgcatac 840  
 184 cccatataaaggaa ggaagggttga atgcataatgc agggcaact ggactggacaa aataatgacca 900  
 185 attctggtaa tatcttctga tctatcgatc acagtcggat atttgtgtc tggcattccc 960  
 186 actgacactc cttaggggaga ggatagtcaat ttcacaggct catgtacaaatg tcctttggg 1020  
 187 aataaaaggat acggttaaaaa aggtttcggtt ttgcacaaag gaactatgtt atggggccgaa 1080  
 188 aggacaaatata gtagggacttc aatgcaggaa ttgcacaaataaaaatcat gaatgttgg 1140  
 189 acacagaaca gtaaaaagacca aatcagaagg caagtgatca ttgataaccc aaatttgtca 1200  
 190 ggatatacgcc gttttttcac attgcgggtt gaactaacaa aaaagggtata gtttagtccc 1260  
 191 ctgttcttcgtt gttgaaatgtt ttagaggttaa acctgaagaa acaacaatat ggaccttcgt 1320  
 192 cagtccttccat gttgtgtgtt ggttagatca taaaattggcc agtttgtcat ggcacgtgg 1380  
 193 agctatttttcccttgacca tagacaagat gtag 1414

196 <210> SEQ ID NO: 10  
197 <211> LENGTH: 26  
198 <212> TYPE: DNA  
199 <213> PROBES

26

201 tggcgacca tggc  
301 <310> SEQ ID NO:

204 <210> SEQ ID NO: 11  
205 <211> LENGTH: 28  
206 <212> TYPE: DNA

28

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208 <400> SEQUENCE: 11  
209 tttcttagact ttaaytgtca wactcytc  
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213 <211> LENGTH: 1

214 <212> TYPE: DNA  
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216 <400> SEQUENCE:

217	atggcgtctc	aaggcaccaa	acgatcttat	gagcagatgg	aaactgtatgg	ggaacgcggag	60
218	aatgcacta	aatcagcagc	atctgtcgga	aggatgttgg	gaggaatcgg	ccggttttat	120
219	gttcagatgt	gtactgagtt	taaattaaac	gaccatgtaa	ggcgcgttat	tcaagaacagc	180
220	ataacaatag	aaaggatgtt	actttcggca	tttcgacgaaa	aaagaaacaaa	gtacctcgag	240
221	gagcatecca	gtgtctggaa	agaccctaaag	aaaacggggag	gccccatata	cagaaggaaaa	300
222	gatggaaat	ggataagaga	actcatcctc	catgataaaag	aggaaatcat	gagggtctgg	360
223	cgtcaggcga	acaatgttga	agatgtctact	gtctgttctt	ccccatatgtat	gatctggcacc	420
224	tccatactca	atgacaccac	ataccaaaga	acaagggtctc	ttgttccgac	ttgggtatggat	480
225	ccccaaatgt	gtctctgtat	gcaaggatca	accctttccac	ggagatctgg	atgtccgggt	540
226	gctcgatcaa	aagggttgg	acaatgata	atggaaactca	tcaggatgtat	caaacgcggg	600

DATE: 10/13/2000  
TIME: 08:27:22

Input Set : A:\Audionnel.app  
Output Set: N:\CRF3\10132000\I677672.raw

VERIFICATION SUMMARY DATE: 10/13/2000  
PATENT APPLICATION: US/09/677,672 TIME: 08:27:23

Input Set : A:\Audonne1.app  
Output Set: N:\CRF3\10132000\I677672.raw

L: 9 M:270 C: Current Application Number differs, Replaced Application Number.  
L: 10 M:271 C: Current Filing Date differs, Replaced Current Filing Date.  
L: 26 M:282 W: Numeric Field Identifier Missing, <213> is required.  
L: 34 M:282 W: Numeric Field Identifier Missing, <213> is required.  
L: 42 M:282 W: Numeric Field Identifier Missing, <213> is required.  
L: 78 M:282 W: Numeric Field Identifier Missing, <213> is required.  
L: 86 M:282 W: Numeric Field Identifier Missing, <213> is required.  
L: 122 M:282 W: Numeric Field Identifier Missing, <213> is required.  
L: 130 M:282 W: Numeric Field Identifier Missing, <213> is required.  
L: 138 M:282 W: Numeric Field Identifier Missing, <213> is required.  
L: 169 M:282 W: Numeric Field Identifier Missing, <213> is required.  
L: 200 M:282 W: Numeric Field Identifier Missing, <213> is required.  
L: 208 M:282 W: Numeric Field Identifier Missing, <213> is required.  
L: 216 M:282 W: Numeric Field Identifier Missing, <213> is required.  
L: 248 M:282 W: Numeric Field Identifier Missing, <213> is required.